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A genome-wide association study of venous thromboembolism identifies risk variants in chromosomes 1q24.2 and 9q

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Summary

Objectives—To identify venous thromboembolism (VTE) disease-susceptibility genes.

Patients/Methods—We performed *in silico* genome wide association (GWAS) analyses using genotype data imputed to ~2.5 million single nucleotide polymorphisms (SNPs) from adults with objectively-diagnosed VTE (n=1503), and controls frequency-matched on age and sex (n=1459; discovery population). SNPs exceeding genome-wide significance were replicated in a separate population (VTE cases, n=1407; controls, n=1418). Genes associated with VTE were resequenced.

Results—Seven SNPs exceeded genome-wide significance ($P < 5 \times 10^{-8}$); four on chromosome 1q24.2 (*F5* rs6025 [Factor V Leiden], *BLZF1* rs7538157, *NME7* rs16861990 and *SLC19A2* rs2038024) and three on chromosome 9q34.2 (*ABO* rs2519093 [*ABO* intron 1], rs495828, rs8176719 [*ABO* blood type O allele]). The replication study confirmed a significant association of *F5*, *NME7*, and *ABO* with VTE. However, *F5* was the main signal on 1q24.2 as only *ABO* SNPs remained significantly associated with VTE after adjusting for *F5* rs6025. This 1q24.2 region was shown to be inherited as a haplotype block. *ABO* resequencing identified 15 novel single nucleotide variations (SNV) in *ABO* intron 6 and the *ABO* 3' UTR that were strongly associated with VTE ($P < 10^{-4}$) and belonged to three distinct linkage disequilibrium (LD) blocks; none were in LD with *ABO* rs8176719 or rs2519093. Our sample size provided 80% power to detect odds ratios=2.0 and 1.51 for minor allele frequencies=0.05 and 0.5, respectively ($\alpha=1 \times 10^{-8}$; 1% VTE prevalence).

Conclusions—Aside from *F5* rs6025, *ABO* rs8176719 and rs2519093, and *F2* rs1799963, additional common and high VTE-risk SNPs among whites are unlikely.

Keywords

venous thromboembolism; deep vein thrombosis; pulmonary embolism; genetics; genome-wide scan; epidemiology

Introduction

Venous thromboembolism, consisting of deep vein thrombosis (**DVT**) and its complication, pulmonary embolism (**PE**), is a common and potentially fatal disease. The overall annual VTE incidence among USA whites is 108 per 100,000 person-years; incidence rates increase exponentially with age for both men and women, and for both DVT and PE.[1] For almost one-quarter of PE patients, the initial clinical presentation is sudden death.[2] Family and twin studies suggest that VTE is highly heritable ($h^2=0.62$) and likely results from multigenic action as well as environmental exposures.[3-5] Several genetic disorders or mutations that affect the regulation of hemostasis have been associated with VTE in small case-control studies or observed in high VTE-risk pedigrees.[6] These include mutations that impair the anticoagulant pathway, up-regulate (e.g., prothrombin G20210A) or impair downregulation of the procoagulant pathway (e.g., Factor V Leiden), downregulate fibrinolysis, and up-regulate innate immunity. In a SNP-based candidate gene, case-control study, we tested genetic variation within all known important components of the anticoagulant, procoagulant, fibrinolytic and innate immunity pathways for an independent association with VTE and found one or more SNPs within *ABO*, *F2*, *F5*, *F11*, *KLKB1*, *SELP* and *SCUBE1* were significantly associated with VTE, including Factor V Leiden (*F5* rs6025 T [minor] allele), prothrombin G20210A, ABO non-O blood type (*ABO* rs8176719, odds ratio [**OR**]=1.47, $P=5.68 \times 10^{-12}$), and a novel association with *ABO* rs2519093 (**OR**=1.68, $P=8.08 \times 10^{-16}$) that was independent of blood type.[7] A GWAS confirmed associations of VTE with Factor V Leiden and with *ABO* loci (blood groups non-O and A2), [8] and a second GWAS with a larger sample size and more dense genome-wide scan genotype data found associations of VTE with the *F11* and *FGG* loci.[9] We hypothesized that genes within other pathways also are VTE disease-susceptibility genes. To test this hypothesis, we performed a genome-wide association study on the same VTE case-control (discovery) population used for our candidate gene study, and replicated all SNPs exceeding genome-wide significance in a separate VTE case-control (replication) population. Finally, we performed gene resequencing in order to identify potentially “causative” genetic variation in LD with haplotype-tagged SNPs that were associated with VTE.

Materials and Methods

Discovery population

The discovery study population consisted 1503 VTE cases and 1459 controls (Supplementary Table 1) from a candidate gene (**CG**) study, as previously described.[7] A subset of the CG study, 1270 VTE cases and 1302 controls, who consented to sending their leukocyte genomic DNA outside of the Mayo Clinic, and newly recruited cases and controls, have genome-wide scan (**GWS**) genotype data. The Mayo Clinic IRB approved the study protocol as well as the data sharing protocol administered through Database for Genotypes and Phenotypes (**dbGAP**).

Genotyping

Candidate Gene (CG) study—Leukocyte genomic DNA was extracted, quantified and diluted to the appropriate concentration for Illumina Infinium iSelect genotyping within the Genotyping Core Laboratory of the Mayo Clinic Advanced Genomics Technology Center, as previously described.[7] Genotyping controls included 2% sample replicates and a CEPH trio for quality control. In addition, case and control DNA sample addresses were randomly assigned across both the 96-well plate as well as the 12-address iSelect BeadChip, ensuring approximately equal numbers of case and control DNA samples by each stratum to avoid potential plate and chip effects, respectively. Genotyping results from high-quality control DNA (SNP call rate 95%) were used to generate a cluster algorithm. Of the 14,612 SNPs

submitted to Illumina from 764 genes within the anticoagulant, procoagulant, fibrinolytic and innate immunity pathways, 1,585 SNPs (covering 1,100 LD bins) failed manufacture, leaving 13,027 successfully genotyped SNPs. Four additional SNPs were custom genotyped on TaqMan, leaving 13,031 SNPs for analysis.

Genome-wide Scan (GWS) study—The Center for Inherited Disease Research (CIDR), one of two genotyping centers supported by the Gene, Environment Association Studies Consortium (GENEVA) consortium,[10] genotyped DNA samples using the Illumina Human660-Quad v.1_A BeadChip (Illumina) and DNA from a subset of CG cases and controls that consented to sending their DNA outside Mayo. Similar to the CG study, case and control DNA sample addresses were randomly assigned across 96-well plates provided by CIDR while ensuring roughly equal percentages of cases and controls within each plate. Genotype clusters for each SNP were determined using the Illumina BeadStudio Module (version 3.3.7), and combined intensity data from 96.6% of samples were used to define clusters and call genotypes. Overall, 99.9% of samples attempted (2,597 of 2,600 total) passed quality-control standards. Genotypes were not called if the quality score from BeadStudio was <0.15 . Both the mean SNP call rates and the mean sample call rates were 99.9%. Genotypes were released for 560,816 SNPs (99.88% of those attempted). Genotypes were not released for autosomal SNPs with call rates $<85\%$, >1 HapMap replicate error, $>9\%$ difference in call rate between genders, <0.2 cluster separation or $>11\%$ difference in heterozygote frequency. Duplicate samples from both HapMap and the study were included on each plate. Four HapMap trios (parents and child) were included to detect Mendelian inheritance errors (i.e., whether the alleles are incorrectly passed from each parent to the child). Reproducibility rates in the raw data were 99.99% among 32 duplicated study subjects. The genotype concordance in the 134 HapMap control samples was 99.8%.

Quality-control steps

For both CG and GWS studies, four main categories of quality-control flags were set for autosomal SNPs: (i) unacceptably high rates of missing genotype calls ($>5\%$), (ii) low minor allele frequency (MAF) (<0.005), (iii) unacceptably high rates of Mendelian errors (>1) and (iv) deviation from Hardy-Weinberg equilibrium (HWE, $P < E-05$). For the CG study, of the SNPs performing well (12,477/13,031) 181 SNPs were excluded due a $MAF < 0.005$ ($n=127$) or a call rate <0.95 ($n=54$), leaving 12,296 SNPs (covering 10,456 bins) for the association analysis. For the GWS study, we flagged 1,965 SNPs with $>5\%$ missing genotypes. A total of 1,683 (1,115/1,135) SNPs were flagged overall (cases/controls) for HWE deviation at $P < E-05$.

Population stratification

To test for “cryptic relatedness” in our population, we conducted a population structure analysis on all participating subjects to document genetic diversity among our population. Using 494 Ancestry Informative Markers (AIMS) available on both our candidate gene and GWA studies,[11] we ran STRUCTURE on 2962 participants.[12] The triangle plot provided a graphical representation of genetic structure of our participants plus 209 unrelated individuals from HapMap phase II populations (Yorubans [YRI]; European-Americans from the CEPH collection [CEU]; Chinese from Beijing [CHB]; and Japanese from Tokyo [JPT]), giving a clear sense of how our participants fall among the HapMap reference populations (Supplementary Figure 1).

Replication population

SNPs exceeding genome-wide significance in the discovery population and not in LD within a gene were genotyped in a separate replication population of 2,825 individuals (VTE cases,

n=1407; controls, n=1418; Supplementary Table 3). Replication study leukocyte genomic DNA samples were largely from Olmsted County, MN, USA residents with objectively-diagnosed incident VTE over the 45-year period, 1966-2010, and previously-matched Olmsted County resident controls, as previously described.[13-15] The replication case and control sample size was augmented by leukocyte DNA from non-Olmsted County Mayo Clinic patients identified as described for the CG study population.[7]

DNA resequencing

We selected a subset of the discovery VTE cases and controls for resequencing to take advantage of the joint configuration of two *ABO* SNPs independently associated with VTE, rs8176719 (*ABO* exon 6 deletion determining type O blood group) and rs2519093 (*ABO* intron 1 tag SNP).[7] We randomly sampled 82 cases and 14 controls within 3 of the 9 potential allele frequency cells (Supplementary Figure 8). The rs8176719 alleles are --/-- (deletion is the major allele), --/G, and G/G (G is the minor allele). The rs2519093 alleles are G/G (G is the major allele), A/G, and A/A (A is the minor allele). For each SNP, the genotypes are represented as 0, 1, or 2 copies of the minor allele. We represented the joint allelic configuration of the two SNPs with the number of copies of the rs8176719 minor allele given first as 0/0 (both with 0 copies of the minor allele), 0/1, 0/2 (0 copies of the rs8176719 minor allele), 1/0 (1 copy of the minor rs8176719 allele), 1/1, and 1/2, and 2/0 (2 copies of the rs8176719 SNP minor allele and 0 copies of the rs2519093 minor allele), 2/1, and 2/2. From Supplementary Figure 8, one observes discrepancies between cases and controls at the 0/0, 1/1 and 2/2 combinations. We randomly sampled from these three combinations, taking one third of the case series. For each SNP, we had 28 cases with 0/0 copies of the minor allele, 27 cases with 1/1 copies of the minor allele; and 27 cases with the combination of 2/2 copies of the minor allele. We compared these 82 cases with 14 controls that do not have any of these combinations.

Capture of the target genomic regions was performed using the Agilent custom eArray. The capturing probes (baits) of 120 bases in length were designed based on the paired-end sequencing protocol with a tiling frequency of 3x. The standard repeat masked regions were avoided based on the definition in the UCSC genome database. The repeat regions are mostly in intronic regions of the genes.

Sequencing was performed using Illumina's HiSeq 2000 sequencer. Twelve samples were multiplexed in each lane of the 8-lane flow cell, and a total of 96 samples (82 VTE cases and 14 controls) were sequenced. The read qualities were examined by FastQC (<http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc>) which generates QC matrix from the FASTQ files including per-base sequence qualities, per-sequence quality scores, per-base nucleotide content, and sequence duplication levels. The FastQC tool also provides warnings for parameters failing to pass QC thresholds. The paired-end 100-base reads were aligned to human genome build 36 using Burrows Wheeler Aligner (BWA)[16] allowing 4% of editing distance within a seed length of 32. If the sequence duplication levels failed to pass the FastQC threshold, the duplicated reads were removed using the SAMtools's rmdup method. [17] The BWA alignment was then cleaned up and improved using the Genome Analysis ToolKit (GATK)[18] by recalibration and local re-alignments. SNVs were called using SNVMix[19] with a cut-off probability score of 0.8 based on our preliminary testing using a HapMap CEPH subject sequenced by the 1000 genome project (data not shown), and INDELs were called by GATK with default parameters setting.

The read depths of each of the A, C, G, T bases at each variant position, as well as the average mapping quality score were provided by curating the BAM pile-up files using SAMtools.[17] If an identified SNV was a known variant from dbSNP or 1000 Genomes Project, the allele frequencies of CEU, YRI, and CHB/JPT populations from HapMap and

1000 Genome Project were provided. Both SNVs and INDELs were annotated by batch submission to the SeattleSeq server, and for SNVs additional annotations were acquired using a locally or cloud installed SIFT.[20] The SNVs or INDELs within a user defined distance (default: 5 bases) to exon-intron boundaries were flagged as potential splice variants and the corresponding transcript IDs are provided.

Information was reported on genes hosting SNVs and INDELs, including (i) the KEGG pathway(s) (<http://www.genome.jp/kegg>) to which the gene belongs; and (ii) tissue expression specificity of the gene.

Statistical methods

GWS (Illumina 660Q; 557,112 SNPs) and CG (n=764 genes relevant to the anticoagulant, procoagulant, fibrinolytic and innate immunity pathways; n=12,551 SNPs) genotypes from the discovery population VTE cases (objectively-diagnosed; no cancer, catheter or antiphospholipid antibodies; n=1503) and controls (frequency-matched on case age, gender, race, MI/stroke status; n= 1459) were merged and imputed to ~2.5 million SNPs (i.e., *in silico* genotypes) with MACH using HapMap Phase II (60 CEU).[21] All genetic coordinates in tables and figures refer to HapMap release 22 build 36. In regions where no candidate gene genotypes were available, only subjects with GWS data were used for the imputation.

The primary outcome was VTE status, a binary measure. The covariates were age at interview or blood sample collection, sex, stroke/MI status and USA state of residence (Supplementary Table 1). We tested for an association between each SNP and VTE using unconditional logistic regression, adjusting for age, sex, stroke/MI status and USA state of residence using PLINK v 1.07.[22] A similar analysis was performed for the replication study and the covariates were age at interview or blood sample collection, sex and USA state of residence (Supplementary Table 3). Haplotype analyses were performed on the 25 chromosome 1q.24.2 SNPs most significantly associated with VTE, considering 25- and 10-SNP-sliding-windows, as implemented in PLINK v 1.07.[22] Novel *ABO* SNVs identified by resequencing were tested for an association with VTE using age-, sex-adjusted unconditional logistic regression and Fisher's Exact Test. Population attributable risk (**PAR**) was estimated for F5 rs6025 (Factor V Leiden), F2 rs1799963 (prothrombin G20210A) and *ABO* blood type haplotype, as previously performed.[7]

VTE prevalence was estimated using the resources of the Rochester Epidemiology Project which has mapped Olmsted County, MN, USA residency for over 500,000 people from 1/1/1966 to 12/31/2010. All Olmsted County residents with objectively-diagnosed, incident VTE over the 40-year period, 1966-2005, have been followed forward in time until death or last follow-up. VTE point prevalence was recorded for 1/1/2006 using these data and adjusted to the USA white population data from the 2000 Census.

Results

Discovery *in silico* GWAS results

Among the 1503 VTE cases and 1459 controls in the discovery population, the age and sex distributions were similar between cases and controls; however we found a significant difference between VTE cases and controls for prior stroke or myocardial infarction (**stroke/MI**); and USA state of residence (Supplementary Table 1). From the population stratification analysis, 98.64% of samples were classified as European and 1.36% as "other" ancestry (includes individuals of mixed ancestry; Supplementary Figure 1). Since age, sex, prior stroke or myocardial infarction have been shown or suggested to be risk factors for

VTE,[1] and due to the significant difference between VTE cases and controls regarding USA state of residence, we adjusted for these four characteristics in the logistic regression analyses.

After adjusting for age, sex, stroke/MI and USA state of residence, 39 SNPs exceeded genome-wide significance ($P < 5 \times 10^{-8}$; Figure 1A and Supplementary Table 2); *F2* rs1799963 (prothrombin G20210A) was borderline significant ($OR=2.46$, $P=1.7 \times 10^{-6}$). The quantile-quantile plot of the expected vs. observed genome-wide $-\log(P\text{-values})$ (Supplementary Figure 2) shows the impact of chromosome regions 1q24.2 and 9q on VTE risk. Table 1 shows the association results for significant SNPs not in LD within a gene (*F5* rs6025, *BLZF1* rs7538157, *NME7* rs16861990, *SLC19A2* rs2038024, and *ABO* rs2519093, rs8176719 [ABO blood type non-O] and rs495828).

Replication and combined results findings

In the separate replication population consisting of 1407 VTE cases and 1418 controls, no significant difference was found between age, sex, and USA state of residence (Supplementary Table 3). Because *BLZF1* rs7538157 was in high LD with *F5*, *SLC19A2* and *ATP1B1*, the *BLZF1* SNP (rs7538157) was replaced by *ATP1B1* rs12061601 (Figure 1B). After adjusting for age, sex and USA state of residence, *F5* rs6025 ($P=1.4 \times 10^{-12}$), *NME7* rs16861990 ($P=4.9 \times 10^{-9}$), and *ABO* rs2519093 ($P=1.2 \times 10^{-17}$), rs495828 ($P=2.4 \times 10^{-17}$) and rs8176719 ($P=5.7 \times 10^{-16}$), were significantly associated with VTE, while *ATP1B1* rs12061601 ($P=0.02$), *F2* rs1799963 ($P=0.03$) and *SLC19A2* rs2038024 ($P=0.09$) were marginally associated (Table 2a). All replicated SNP ORs were in the same direction and of similar magnitude as that of the discovery population.

These SNPs cluster in two genomic regions located on chromosome 1q24.2 (Figure 1B) and on chromosome 9q (Figure 1C). Chromosome 1q24.2 and 9q LD patterns observed in controls are shown in Supplementary Figures 3 and 4, and the ORs and respective 95% confidence intervals for an association of SNPs in these two genomic regions with VTE are depicted in Supplementary Figures 5 and 6. Since *ATP1B1*, *NME7*, *BLZF1* and *SLC19A2* are in close proximity to *F5*, we repeated the association analysis including the *F5* rs6025 T (minor) allele (Factor V Leiden) as a covariate and found that only the *ABO* SNPs remained significantly associated with VTE at the genome-wide level. Similarly, in the replication study only the *ABO* SNPs and *SLC19A2* rs2038024 remained significantly associated with VTE after adjusting for *F5* rs6025 T. Although *SLC19A2* rs2038024 was marginally associated with VTE, the OR was in the opposite direction from that of the discovery population, suggesting a spurious association (Table 2b).

Receiver Operator Characteristic areas under the curve (AUC), calculated individually and jointly using all significant SNPs, were not different for covariates (age, sex, stroke/MI and USA state of residence) plus *F5* rs6025 T (AUC=0.653) compared to covariates plus *F5* rs6025 T, *ATP1B1* rs12061601, *NME7* rs16861990 and *SLC19A2* rs2038024 (AUC=0.653), while addition of *ABO* SNPs did increase the AUC (AUC=0.675; Figure 2).

Haplotype analysis results

Haplotype analysis of the 25 chromosome 1q24.2 SNPs (including *ATP1B1*, *NME7*, *BLZF1*, *C1orf114*, *SLC19A2*, *F5* and *SELP*; Figure 1B and Supplementary Table 4) most significantly associated with VTE showed that only the two haplotypes containing *F5* rs6025 T were significantly associated with VTE (Table 3). Together, these data suggest that this chromosome 1q24.2 region is inherited as a haplotype block of ~0.52mb. Among all *F5* rs6025 T carriers ($N=369$; 280 cases and 89 controls; 186 males and 183 females), 235 (63.7%; 177 cases and 58 controls) carriers inherited at least one of these two 1q24.2

haplotypes. The haplotype containing the *F5* rs6025 T and the *SELP* rs3917862 G (minor) alleles slightly increased the association of the haplotype with VTE (OR=3.59) compared to the haplotype containing the *F5* rs6025 T and the *SELP* rs3917862 A alleles (OR=3.16, Table 3). However, a 10-SNP-sliding-window with nine SNPs in *F5* (including the *F5* rs6025 T allele) and one SNP in *SELP* (SNP rs3917862 G [minor] allele) considerably increased the association of this haplotype with VTE (OR=4.55, $P=2.07 \times 10^{-13}$) compared to the association for the haplotype containing the *F5* rs6025 T and *SELP* rs3917862 A alleles (OR=3.09, $P=1.83 \times 10^{-11}$; Supplementary Table 5).

Resequencing results

To further evaluate *ABO* sequence variation for an association with VTE, we performed *ABO* resequencing, including 10 Kb of the flanking regions, using Illumina HiSeq 2000. Excluding the intronic repeat regions, 98% of the targeted area (Supplementary Figure 7) was sequenced with > 20X coverage in 96 samples (82 VTE cases and 14 controls). On average, ~35-40 SNVs and ~5-10 insertion-deletions (**INDELs**) were detected in each sample. Fifteen novel SNVs in *ABO* intron 6 and the *ABO* 3' UTR were associated with VTE (all $P < 10^{-04}$) and belonged to three distinctive LD blocks; none were in LD with *ABO* rs8176719 (blood type O allele) or rs2519093 although *ABO* rs8176746 (blood type A allele) and rs8176747 (blood type B allele) were in moderate LD ($r^2=0.56-0.65$) with novel SNPs in block 3 (Figure 3; Supplementary Table 6). Although *ABO* rs8176746 and rs8176747 did not reach genome wide significance in the primary analysis, a secondary analysis (adjusted for age, sex, stroke/MI and USA state of residence) of the derivation population that considered *ABO* blood type (either haplotype/genotype or phenotype; VTE cases, n=1459; controls, n=1422) found strong associations of *ABO* blood types A (OR=1.64; 95%CI: 1.41, 1.91; $P=7.83 \times 10^{-11}$) and O (OR=0.52; 95%CI: 0.44, 0.60; $P=2.40 \times 10^{-16}$) with VTE, but no association with blood types B (OR=1.15; 95%CI: 0.91, 1.44; $P=0.25$) or AB (OR=1.22; 95%CI: 0.87, 1.70; $P=0.25$; Supplementary Table 7). Finally, a significant, protective, frame-shifting single base (G) deletion of one of three guanines at *ABO* chr9:135120878-80 was found within exon 7. This deletion likely corresponds to *ABO* rs8176750 (*ABO* blood-type A2).

The individual, joint and group population attributable risk (**PAR**) were calculated for the risk genotypes for Factor V Leiden (*F5* rs6025), prothrombin G20210A (*F2* rs1799963), and *ABO* blood type haplotype or genotype (Supplementary Table 8). The highest PAR value was from the *ABO* blood type non-O, followed by *ABO* blood type A, Factor V Leiden, and prothrombin G20210A. The PAR values were very similar between the joint and group estimation methods, with highest joint or group PAR (PAR=0.47) for *ABO* blood type non-O, *F5* rs6025 and *F2* rs1799963).

Discussion

Our most notable finding was the strong association of VTE with three novel and distinctive *ABO* LD blocks that were independent of *ABO* type O blood type. *ABO* encodes for glycosyltransferases responsible for post translational glycosylation of procoagulant FVIII and von Willebrand Factor (**VWF**).^[23] *ABO* O blood group phenotype and genotype (i.e., *ABO* rs8176719) is associated with a decreased risk for VTE,^[7, 8, 24] presumably due to decreased plasma levels of FVIII and VWF.^[25, 26] *ABO*-mediated glycosylation protects VWF from proteolysis by ADAMTS13^[27] such that individuals with type O blood group (homozygous exon 6 *ABO* rs8176719 deletion) and hypoglycosylated VWF have ~25% lower plasma FVIII and VWF levels.^[24, 28]

We previously identified an independent association of an *ABO* intron 1 SNP (rs2519093) with VTE (OR=1.68, $P=8.08 \times 10^{-16}$).^[7] This intronic region does not affect RNA splicing or

harbor any suppressor RNA elements, nor is it close to any other *ABO* variants with known function, including variants in *ABO* exons 6 and 7 that have been variably associated with VTE risk.[29-33] Of the 15 novel *ABO* SNVs found on resequencing, none were in LD with this *ABO* intron 1 SNP (Figure 3; Supplementary Table 6). Consequently, the findings of this study expand on our previous observation and suggest that this *ABO* intron 1 region along with an LD block in *ABO* intron 6 and two LD blocks in the *ABO* 3' UTR play important roles in *ABO* expression and associated VTE risk.

In a secondary analysis, the *ABO* blood type A haplotype was strongly associated with VTE (Supplementary Table 7) as previously described.[31-34] In the limited and select sample (n=96) of our discovery population who underwent *ABO* resequencing, the *ABO* A allele was in moderate LD ($r^2=0.56-0.65$) with SNVs in *ABO* LD block 3 (Figure 3) which potentially could account for the association of these novel block 3 SNVs with VTE. The association of VTE with novel SNVs in *ABO* LD block 2 was independent of blood type A (rs8176747) and O (rs8176719) alleles, and *ABO* rs2519093 (Figure 3). *ABO* LD block 2 may be important for gene regulation due to a potential open chromatin region as reflected by enrichment for multiple epi-genetic markers in the region,(ENCODE: <http://www.genome.gov/10005107>) a transcription factor binding site (ChIP-seq, ENCODE: <http://www.genome.gov/10005107>), and evolutionary conservation (UCSC phatCons[35] and phylo[36] algorithms; Figure 4). In addition, strong evidence from dbEST supports the middle LD block as also lying within a novel transcript, probably an extension of the 3' of *ABO* (dbEST: <http://www.ncbi.nlm.nih.gov/dbEST/>; Figure 4). *ABO* SNV_135116452 was not part of any *ABO* LD block but it was in high LD with SNVs from LD block 3, and in moderate ($r^2=0.54$) LD with the *ABO* blood type A allele (rs8176747; Figure 3). Thus, the association of SNV_135116452 with VTE may also be due to blood type A. Lastly, the SNVs in *ABO* LD block 1 are in low LD with all the other SNVs and SNPs (Figure 3). The associations of SNVs in LD block 1 with VTE are independent of blood type A ($r^2\sim0.27-0.44$) and O ($r^2\sim0-0.02$) alleles, and *ABO* rs2519093 ($r^2\sim0-0.04$; Figure 3).

Our *ABO* resequencing data also support the previously reported association of VTE with *ABO* blood type A2 (*ABO* rs8176750).[8, 31] Although we did not directly genotype *ABO* rs8176750 in either our CG or GWAS studies, one directly-genotyped *ABO* SNP (rs8176704) in strong LD with rs8176750 ($r^2=0.8$) was associated with a significantly reduced risk of VTE (OR=0.78; 95%CI: 0.63, 0.97, $P=0.02$) that was of similar magnitude to that reported for *ABO* blood type A2.[8, 31] The *ABO* rs8176750 deletion results in a frame-shift that abrogates the wild-type stop codon within exon 7 and likely leads to an elongated transcript (Figure 4) and an absent or dysfunctional protein similar to blood type O.

Our second notable finding was the discovery that Factor V Leiden is inherited as a haplotype block that spans seven genes on chromosome 1q24.2, including *ATP1B1*, *NME7*, *BLZF1*, *C1orf114*, *SLC19A2*, *F5* and *SELP*. *F5* encodes for plasma procoagulant Factor(F) V; FV accelerates activation of prothrombin to thrombin by catalyzing assembly of the prothrombinase complex. FV inactivation is key for down-regulating procoagulant activity. Activated Protein C (APC), a serine protease, inactivates FV via cleavage at arginine[R]306, R506 and R679; initial APC cleavage at R506 is required for rapid FV inactivation by APC cleavage at R306 and R679.[37] *F5* rs6025 encodes for substitution of glutamine for R506. [38, 39] Factor V Leiden carriers have normal FV procoagulant activity but impaired FV down-regulation due to “resistance” to cleavage/inactivation by APC.[40, 41] Factor V Leiden is a founder mutation occurring about 30,000 years ago,[42] and is associated with ~3.5-fold increased risk for VTE (lifetime VTE penetrance ~5%).[7, 38, 43]

Our third finding was that the tag SNP *SELP*rs3917862 compounds the risk of VTE among Factor V Leiden carriers. *SELP* encodes for P-Selectin, a membrane glycoprotein with pro-inflammatory activity that mediates the interaction between activated platelets, leukocytes, immune cells and endothelial cells.[44, 45] Cell-surface P-selectin expression and soluble P-selectin concentration are partly controlled by *SELP* genetic variation.[46, 47] Increased soluble P-selectin plasma levels are associated with incident and recurrent VTE.[48, 49] We previously showed that *SELP*rs3917862 was associated with a 1.6-fold increased risk of VTE at a false discovery rate $q = 0.006$. [7] *SELP* is located immediately upstream from *F5* (Figure 1B), and associations between *SELP* haplotypes and VTE have been attributed to high LD with *F5* rs6025 T.[50] In our previous report, while *SELP*rs3917862 was not in high LD with *F5* rs6025 T ($r^2=0.12$, $D'=0.37$), the association of rs3917862 with VTE was no longer significant ($P=0.3$) after controlling for *F5* rs6025 T.[7] Our new analyses indicate that the haplotype containing the *F5* rs6025 T and the *SELP*rs3917862 G (minor) alleles increases the association of the haplotype with VTE (OR=3.59) compared to the haplotype containing the *F5* rs6025 T and the *SELP*rs3917862 A alleles (OR=3.16, Table 3). Furthermore, the association of the haplotype with VTE increases when considering different numbers of SNPs in the sliding window approach (OR=4.55 for 10-SNP-sliding-window with nine SNPs in *F5* and one in *SELP*; Supplementary Table 5). Based on these statistical analyses, we conclude that the *SELP*rs3917862 T allele compounds the risk of VTE associated with *F5* rs6025 T.

Although we found associations of VTE with *ATP1B1*, *NME7*, *BLZF1*, and *SLC19A2*, these associations disappeared in both the discovery and replication populations after controlling for *F5* rs6025 T (Factor V Leiden). *ATP1B1* encodes for a Na⁺/K⁺ ATPase important in endothelial cell and platelet function, *NME7* encodes for a nucleoside-diphosphate kinase important in erythropoiesis and CD4 T-cell activation, *BLZF1* (*JEM-1*) encodes for basic leucine zipper nuclear factor 1 which is important for the response of acute promyelocytic leukemia to retinoic acid, and *SLC19A2* encodes for a thiamine transporter protein (THTR-1) implicated in thiamine-responsive megaloblastic anemia. While the products of these genes are potentially biologically plausible in the causal pathway to VTE, none have been previously associated with VTE. Moreover, ROC curve analyses showed that SNPs within these four genes added no additional information over that provided by patient characteristics and *F5* rs6025 T alone. Thus, we believe it is unlikely that these genes are VTE disease-susceptibility genes.

Our sample size provided 80% power to detect odds ratios of 2.0 and 1.51 for minor allele frequencies (MAF)=0.05 and 0.5, respectively ($\alpha=5 \times 10^{-8}$) based on a 1% prevalence of VTE among USA whites for the year 2000.[51] While single studies or individual-level data meta-analyses with a larger sample size and/or more dense genome-wide scan genotype data may identify additional SNPs that associate with VTE, we believe that aside from *F5* rs6025, *ABO* rs8176719 and rs2519093, and *F2* rs1799963, additional common (i.e., MAF>0.05) and high VTE-risk (i.e., OR>2.0) SNPs among persons of non-Hispanic European ancestry are unlikely.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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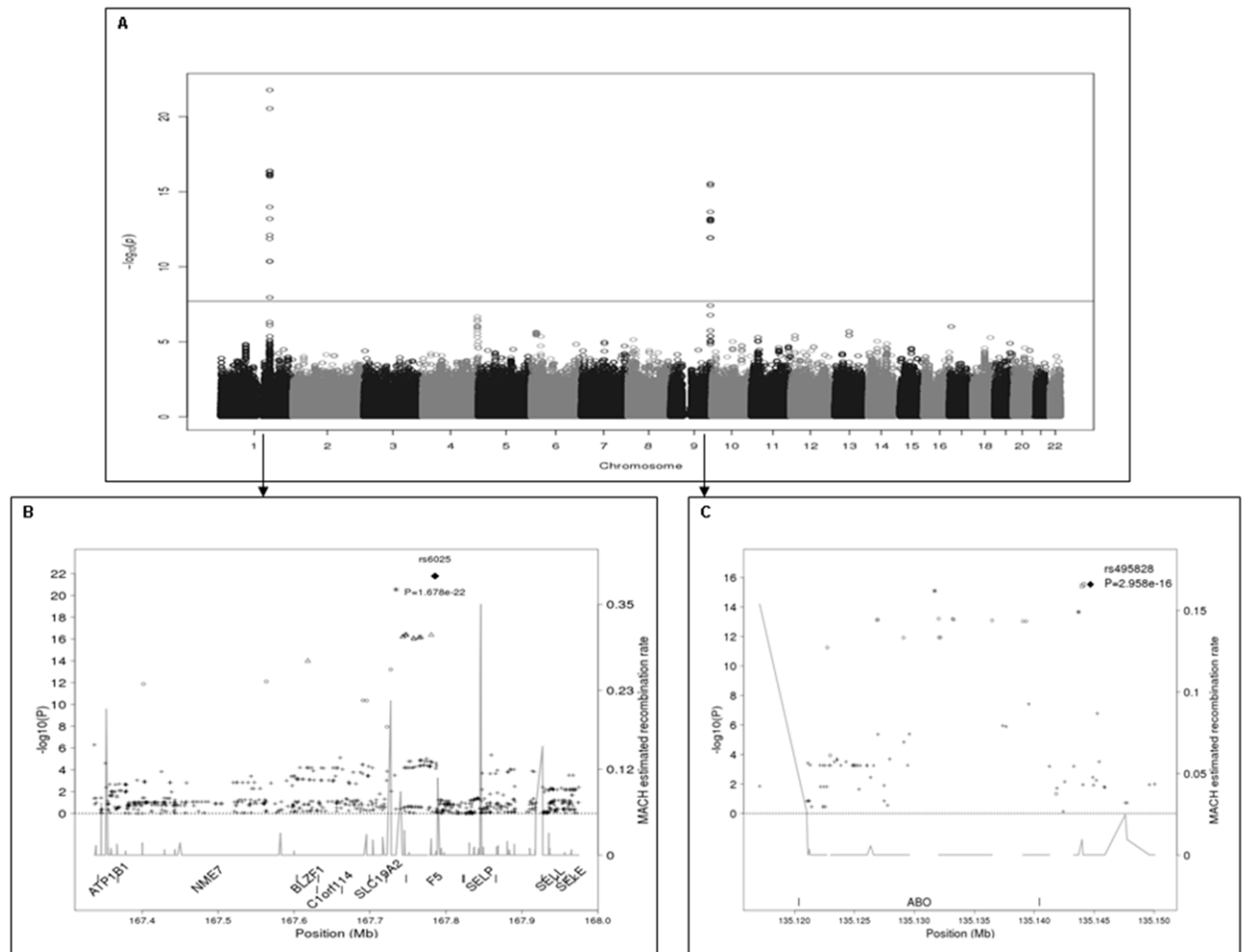


Figure 1.

A. Manhattan plot of $-\log_{10}(P\text{-values})$ from the case-control association analysis on the merged/imputed VTE data assuming an additive genetic model. The horizontal line at 1.99×10^{-8} represents the Bonferroni correction. Figure 1B. Location and linkage disequilibrium for SNPs on chromosome 1q24.2 surrounding *F5*. The black diamond corresponds to *F5* 6025 (Factor V Leiden) the most significant SNP. Figure 1C. Location and linkage disequilibrium for SNPs on chromosome 9q surrounding *ABO*. The black diamond corresponds to the most significant SNP, rs495828. For Figures 1B and 1C, the linkage disequilibrium measure, r^2 , between the most significant SNP and any other SNP in the region is symbol coded; the square, star, triangle, circle, and cross symbols correspond to $r^2 > 0.95$, > 0.8 and 0.95 , > 0.5 and 0.8 , > 0.2 and 0.5 , and 0.2 , respectively.

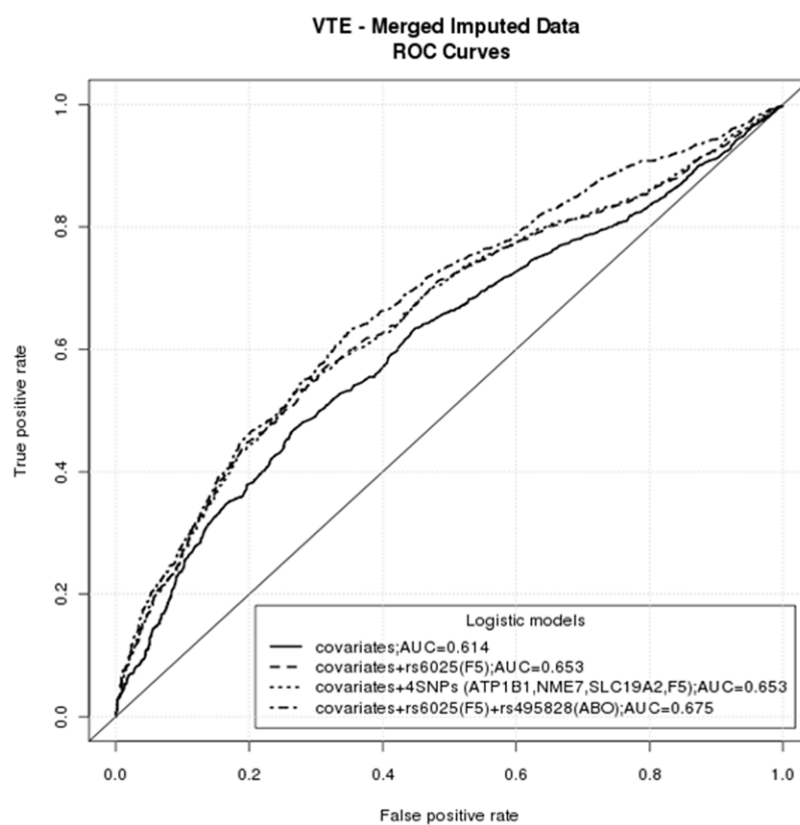


Figure 2.
Receiver Operator Characteristic (ROC) Curve Analyses of Chromosome 1q24.2 and *ABO* SNPs

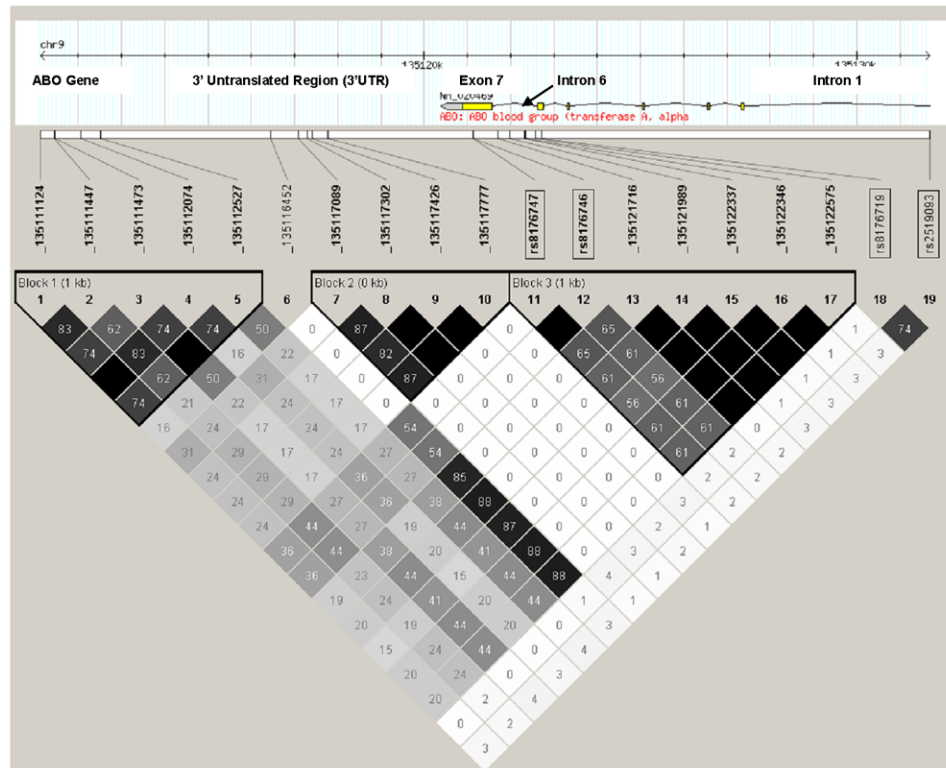


Figure 3.

Linkage disequilibrium (**LD**) between novel *ABO* SNVs identified by resequencing, and *ABO*rs8176474 (blood type A allele), rs8176746 (blood type B allele), rs8176719 (blood type O allele) and rs2519093 (*ABO* intron 1), among 82 VTE cases and 14 controls selected based on *ABO* rs8176719 and rs2519093 genotype (see Methods). The numbers inside each square and the square shading indicate the degree of LD between SNPs and/or SNVs (i.e., black squares with no number indicate complete LD [$r^2=1.0$]; intensity of the gray shading indicates intermediate values between complete LD [$r^2=1.0$] and no LD [$r^2=0.0$], and white squares with 0 number indicate no LD).

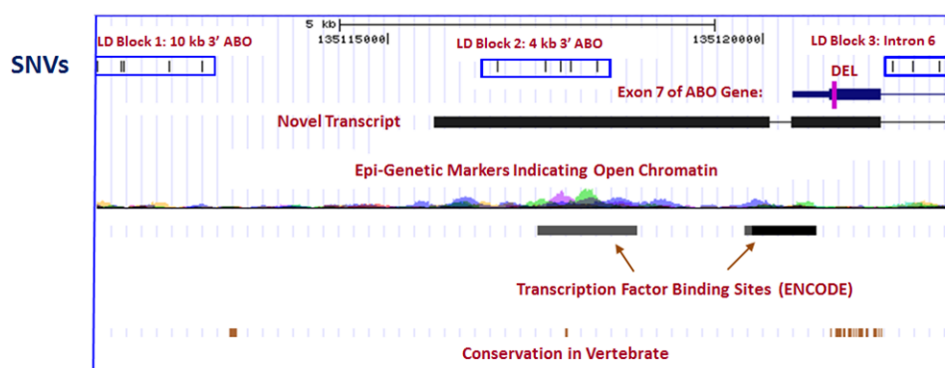


Figure 4. Potential functional roles of *ABO* SNVs identified on resequencing, by LD block or deletion.

Odds ratio and 95% confidence intervals, minor allele, minor allele frequency (MAF) and imputation quality for single nucleotide polymorphisms (SNPs) showing genome-wide significance, adjusted for age, sex, stroke/myocardial infarction status and USA state of residence

Table 1

SNP	Gene	Chromosome	Position [†]	Minor Allele	MAF	OR (95% CI)	P	Imputed (r ²)/Genotyped
SNPs in genes previously reported								
rs6025	<i>F5</i>	1	167785673	T	0.063	3.57 (2.76, 4.60)	1.68E-22	Yes (0.97)/Yes
rs8176719	<i>ABO</i>	9	135122729	G	0.419	1.47 (1.32, 1.64)	5.68E-12	No/Yes [‡]
rs2519093	<i>ABO</i>	9	135131691	A	0.243	1.69 (1.48, 1.91)	8.08E-16	No/Yes [‡]
SNPs in genes not previously reported								
rs7538157	<i>BLZFI</i>	1	167618168	C	0.062	2.69 (2.09, 3.45)	1.04E-14	Yes (0.901)/No
rs16861990	<i>NME7</i>	1	167401751	C	0.099	2.02 (1.66, 2.45)	1.69E-12	Yes (0.932)/Yes [§]
rs2038024	<i>SLC19A2</i>	1	167722606	C	0.177	1.53 (1.32, 1.78)	1.12E-08	Yes (0.893)/Yes [§]
rs495828	<i>ABO</i>	9	135144688	T	0.272	1.65 (1.46, 1.86)	2.96E-16	Yes (0.988)/Yes [§]

[†]NCBI build 36 of the human genome

[‡]Genotype available in all subjects through the candidate gene data set.

[§]Genotype available in only 2570 subjects (87% of our combined samples) through the GWA data set

Table 2

a. Replication odds ratio and 95% confidence intervals, minor allele, minor allele frequency (MAF; overall and by case/control status) using 2,825 subjects (1407 cases and 1418 controls), adjusted for age, sex and USA state of residence

SNP	Gene	Chromosome	N	MAF	MAF - cases	MAF - controls	OR (95%CI)	P
rs6025	<i>F5</i>	1	2543	0.060	0.086	0.035	2.56 (1.97, 3.32)	1.40E-12
rs12061601	<i>ATP1B1</i>	1	2521	0.139	0.151	0.126	1.21 (1.03, 1.43)	0.02
rs16861990	<i>NME7</i>	1	2559	0.097	0.122	0.071	1.79 (1.47, 2.18)	4.89E-09
rs2038024	<i>SLC19A2</i>	1	2603	0.172	0.182	0.162	1.13 (0.98, 1.31)	0.09
rs2519093	<i>ABO</i>	9	2599	0.235	0.289	0.182	1.80 (1.58, 2.07)	1.15E-17
rs495828	<i>ABO</i>	9	2627	0.261	0.317	0.205	1.73 (1.52, 1.96)	2.38E-17
rs8176719	<i>ABO</i>	9	2532	0.416	0.476	0.357	1.63 (1.45, 1.84)	5.62E-16
rs1799963	<i>F2</i>	11	2620	0.019	0.024	0.015	1.69 (1.06, 2.41)	0.03

b. Replication odds ratio and 95% confidence intervals using 2,825 subjects (1407 cases and 1418 controls), adjusted for age, sex, USA state of residence and *F5* rs6025 T allele (Factor V Leiden)

SNP	Gene	N	MAF	MAF-Cases	MAF-Controls	OR (95%CI)	P
rs12061601	<i>ATP1B1</i>	2477	0.137	0.150	0.125	0.92 (0.76, 1.10)	0.35
rs16861990	<i>NME7</i>	2505	0.097	0.123	0.071	1.17 (0.89, 1.54)	0.25
rs2038024	<i>SLC19A2</i>	2474	0.170	0.178	0.163	0.77 (0.65, 0.92)	0.004
rs2519093	<i>ABO</i>	2474	0.235	0.289	0.181	1.85 (1.61, 2.13)	1.37E-17
rs495828	<i>ABO</i>	2501	0.261	0.317	0.205	1.76 (1.54, 2.01)	3.60E-17
rs8176719	<i>ABO</i>	2477	0.416	0.474	0.359	1.58 (1.40, 1.78)	9.75E-14
rs1799963	<i>F2</i>	2485	0.019	0.023	0.015	1.71 (1.12, 2.63)	0.014

Haplotype analysis of the 25 most significant chromosome 1q24.2 SNPs adjusted for age, sex, stroke/myocardial infarction and USA state of residence.

Table 3

Haplotype ^{†‡§}	F	OR	STAT	P
TATAGGTAGAGCTATGCAGCATGC ^{<u>A</u>}	0.136	0.80	7.65	0.006
TATAGGTAGAGCTATGCAGCAGGC ^{<u>A</u>}	0.447	0.92	2.02	0.16
TATAAGTAGAGCTATGCAGCATGC ^{<u>A</u>}	0.0795	0.82	3.68	0.06
TATAAGTAGAGCTATGCAGCAGGC ^{<u>A</u>}	0.0273	0.83	1.04	0.31
CCCCAACCCAGAACTACGGATCGATG	0.0185	3.59	28.9	7.46E-08
TATAAAGTCAAAACTACGGATCGAC ^{<u>A</u>}	0.0127	1.04	0.0313	0.86
CCCCAACCCAGAACTACGGATCGAT ^{<u>A</u>}	0.0227	3.16	29.2	6.55E-08
CATAGGTAGAGCTATGCAGCAGGC ^{<u>A</u>}	0.029	0.97	0.0266	0.87
TATAGGTAGAGCTATGCAGCAGGCC ^{<u>G</u>}	0.0211	1.07	0.109	0.74
TATAAAGTCAAGCTATGCAGCATGC ^{<u>A</u>}	0.0196	0.89	0.385	0.54
TCCAAACAGAGCTATGCAGCAGGCC ^{<u>A</u>}	0.0129	0.73	1.51	0.22
TATAAAGTCGAGCTATGCAGCAGGC ^{<u>A</u>}	0.0162	1.27	1.15	0.28

[†]The first SNP of the haplotype is *ATP1B1* rs12061601, and the last SNP of the haplotype is *SELP* rs3917862

[‡] Allele in bold is *F5* rs6025 (T is the minor allele [Factor V Leiden])

[§] Underlined allele is *SELP* rs3917862 (G is the minor allele)